

FIG. 1

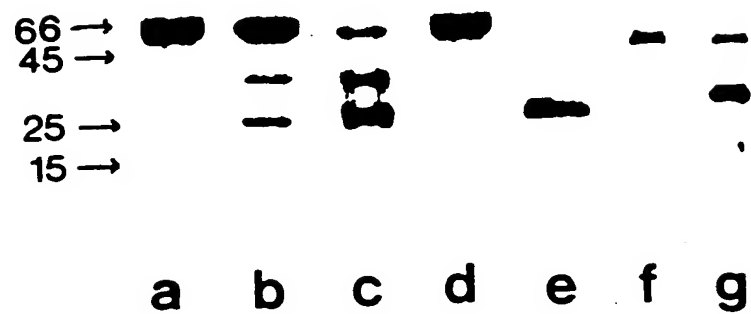


FIG. 2a

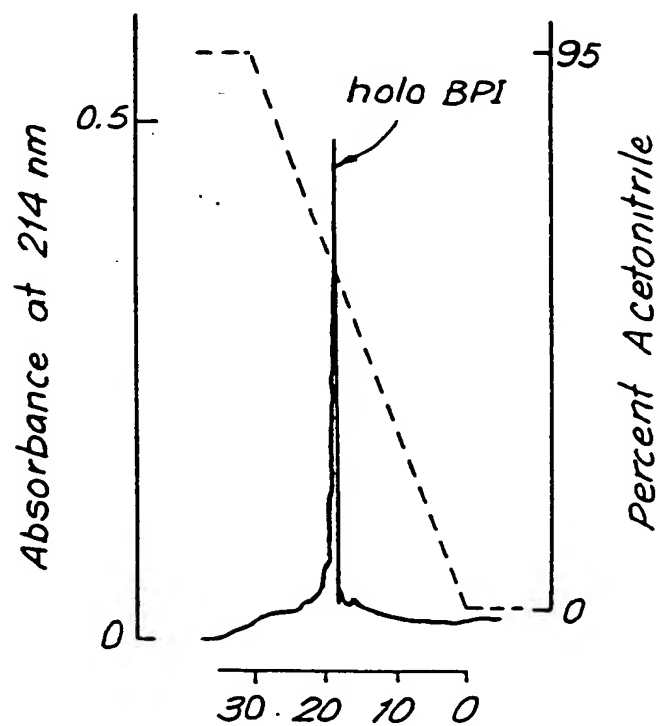


FIG. 2b

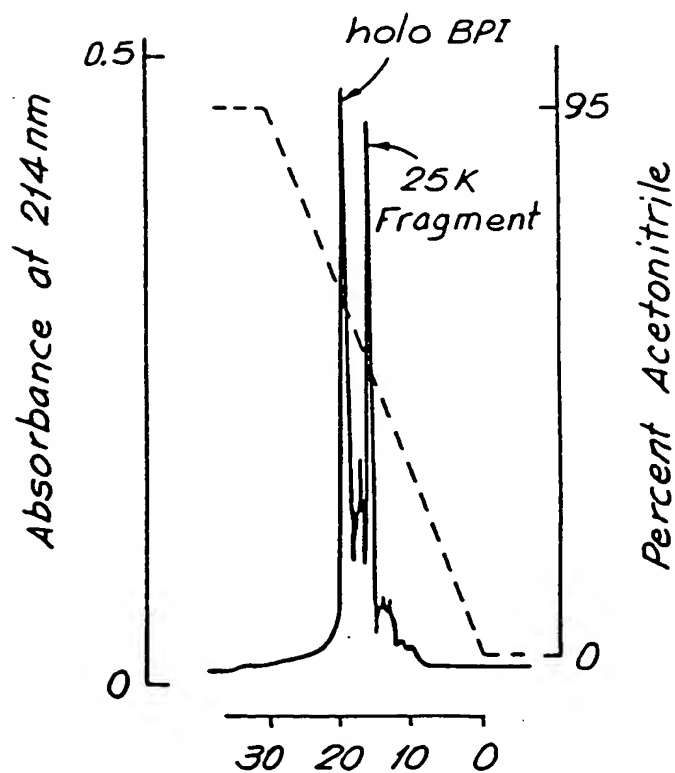


FIG. 3A

Bacterial Viability

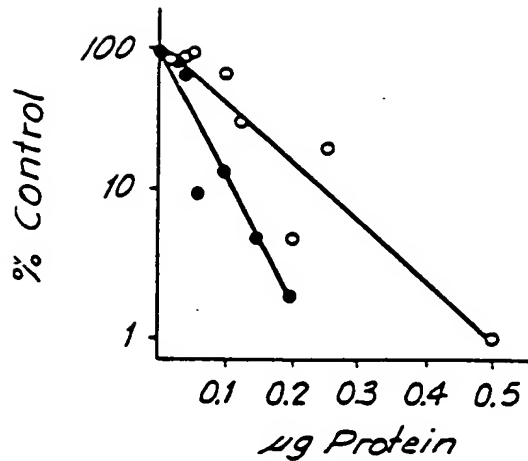


FIG. 3B

*^{14}C -Amino Acid Incorp.
(- Actinomycin D)*

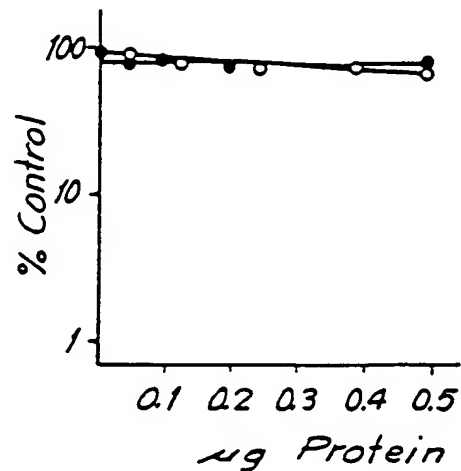


FIG. 3C

*^{14}C -Amino Acid Incorp.
(+ Actinomycin D)*

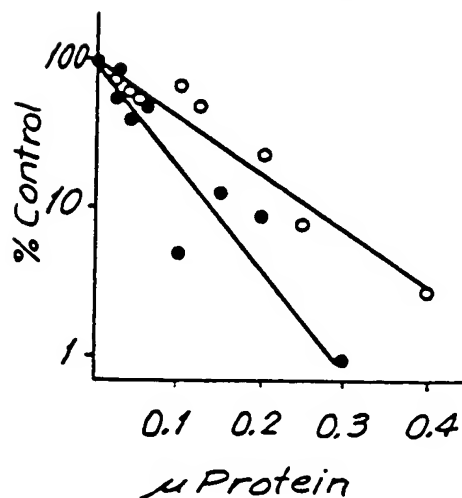


FIG. 3D

Phospholipid Hydrolysis

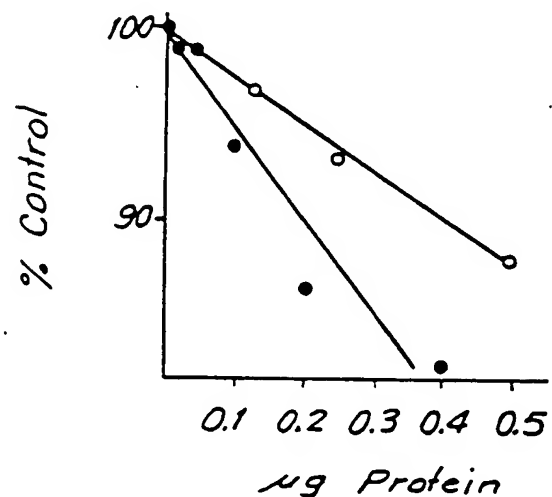


FIG. 4

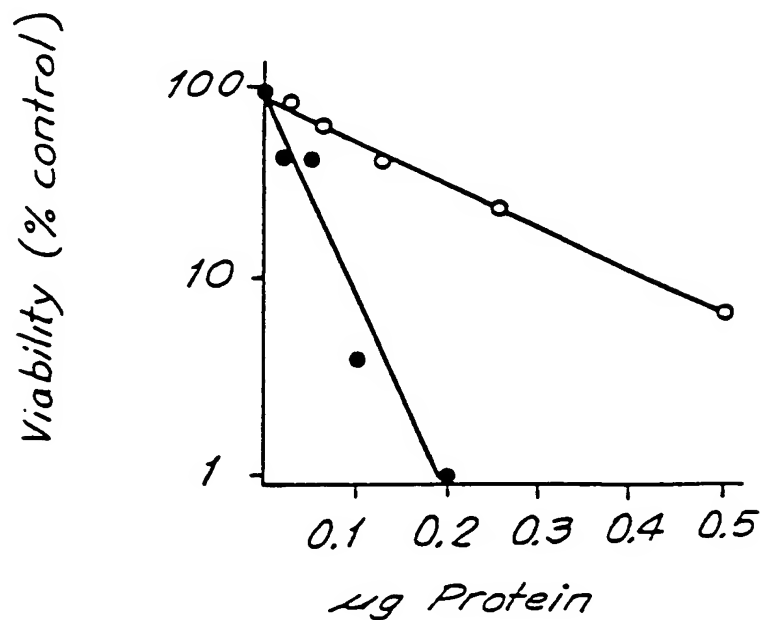


FIG. 5

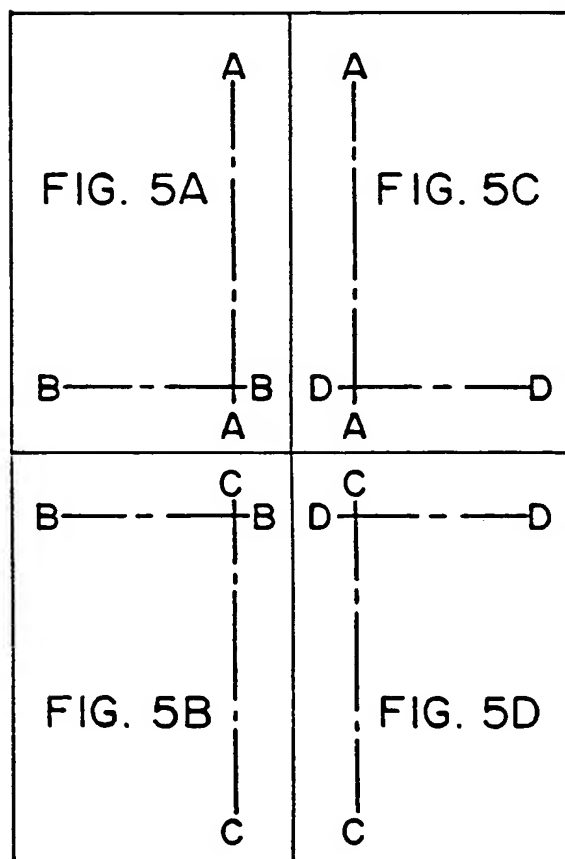


FIG. 5A

1 CAGGCCTTGAGGTTTTGGCAGCTCTGGAGG met arg glu asn
-30 ATG AGA GAG AAC

82 CTG ATG GTG CTC GTC GCC ATA GGC ACC GCC GTG ACA
-10 leu met val leu val ala ile gly thr ala val thr

157 AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC
20 Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala

232 TAC TCA GAC AGC TTT AAG ATC AAG CAT CTT GGG AAG
40 Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys

307 CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT
70 Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn

382 ATC AGC GGG AAA TGG AAG GCA CAA AAG AGA TTC TTA
90 Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe Leu

457 TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT AAC CCC
120 Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro

532 AGC CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG
140 Ser His Ile Asn Ser Val His Val His Ile Ser Lys

607 ATT GAG TCT GCG CTT CGA AAC AAG ATG AAC AGC CAG
170 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln

682 CAA CCT TAT TTC CAG ACT CTG CCA GTA ATG ACC AAA
190 Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys

757 CCT CCA GCA ACC ACG GCT GAG ACC CTG GAT GTA CAG
220 Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln

832 CCT CCC TTT GCT CCA CCA GTG ATG GAG TTT CCC GCT
240 Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala

B

B

A

FIG. 5B

Position	1	2	3	4	5	6	7	8	9	10	11	12
	270											
907	Phe	Phe	Asn	Thr	Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala
	TTC	TTC	AAC	ACA	GCC	GGG	CTT	GTA	TAC	CAA	GAG	GCT
	290											
982	Lys	Glu	Ser	Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	Phe
	AAG	GAG	TCC	AAA	TTT	CGA	CTG	ACA	ACC	AAG	TTC	TTT
	320											
1057	Met	Lys	Ile	Gln	Ile	His	Val	Ser	Ala	Ser	Thr	Pro
	ATG	AAG	ATA	CAG	ATC	CAT	GTC	TCA	GCC	TCC	ACC	CCG
	340											
1132	Pro	Ala	Val	Asp	Val	Gln	Ala	Phe	Ala	Val	Leu	Pro
	CCT	GCC	GTG	GAT	GTC	CAG	GCC	TTT	GCC	GTC	CTC	CCC
	370											
1207	Thr	Thr	Gly	Ser	Met	Glu	Val	Ser	Ala	Glu	Ser	Asn
	ACA	ACT	GGT	TCC	ATG	GAG	GTC	AGC	GCC	GAG	TCC	AAC
	390											
1282	Glu	Leu	Lys	His	Ser	Asn	Ile	Gly	Pro	Phe	Pro	Val
	GAA	CTG	AAG	CAC	TCA	AAT	ATT	GGC	CCC	TTC	CCG	GTT
	420											
1357	Leu	Val	Leu	Pro	Arg	Val	Asn	Glu	Lys	Leu	Gln	Lys
	CTT	GTG	CTG	CCC	AGG	GTT	AAC	GAG	AAA	CTA	CAG	AAA
	440											
1432	Asn	Val	Val	Leu	Gln	Pro	His	Gln	Asn	Phe	Leu	Leu
	AAC	GTA	GTG	CTT	CAG	CCT	CAC	CAG	AAC	TTC	CTG	CTG
1511	GGGGGCTGTCAGCCGCACCTGTTCTGATGGGCTGTGGGGCACCGGC											
1611	TTCTTCGACTCAGATTCAGAAATGATCTAAACACGAGGAAACATTAT											
1711	GCTAAGGCTGCAGAGATATTTCTCCAGGAATCGTGTTTCAATTGTA											
1811	GTG---poly-A tail											

FIG. 5C

A

met ala arg gly pro cys asn ala pro arg trp val ser
ATG GCC AGG GGC CCT TGC AAC GCG CCG AGA TGG GTG TCC

1 -20 10

ala ala Val Asn Pro Gly Val Val Val Arg Ile Ser Gln
GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC TCC CAG

30

Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp
GCT CTG CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC

50 60

Gly His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe
GGG CAT TAT AGC TTC TAC AGC ATG GAC ATC CGT GAA TTC

80

Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys
GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG

100 110

Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met
AAA ATG AGC GGC AAT TTT GAC CTG AGC ATA GAA GGC ATG

130

Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser
ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC

150 160

Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
AGC AAA GTC GGG TGG CTG ATC CAA CTC TTC CAC AAA AAA

180

Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys Leu
GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG CTG

200 210

Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu Val Ala
ATA GAT TCT GTG GCT GGA ATC AAC TAT GGT CTG GTG GCA

230

Met Lys Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro
ATG AAG GGG GAG TTT TAC AGT GAG AAC CAC CAC AAT CCA

250 260

Ala His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr
GCC CAT GAC CGC ATG GTA TAC CTG GGC CTC TCA GAC TAC

D

FIG. 5D

280
Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro
GGG GTC TTG AAG ATG ACC CTT AGA GAT GAC ATG ATT CCA

300 310
Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn
GGA ACC TTC CTA CCT GAG GTG GCC AAG AAG TTT CCC AAC

330
Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr
CCA CAC CTG TCT GTG CAG CCC ACC GGC CTT ACC TTC TAC

360
Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
AAC TCC TCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC

380
Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu Leu
AGG CTT GTT GGA GAG CTC AAG CTG GAT AGG CTG CTC CTG

400 410
Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val Pro Ile
GAA TTG CTG CAG GAT ATC ATG AAC TAC ATT GTA CCC ATT

430
Gly Phe Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr
GGC TTC CCT CTC CCG ACG CCG GCC AGA GTC CAG CTC TAC

450
Phe Gly Ala Asp Val Val Tyr Lys
TTC GGT GCA GAC GTT GTC TAT AAA TGA AGGCACCAGGGGTGCC

TGCCTTTCCCCAGGGAATCCTCTCCAGATCTTAACCAAGAGCCCCTTGCAAAC
TCATTGGAAAAGTGCATGGTGTGTATTTTAGGGATTATGAGCTTCTTTCAAGG
ACCAAGAAATTTCCATTTGTGCTTCATGAAAAAACTTCTGGTTTTTTTCAT

FIG. 6

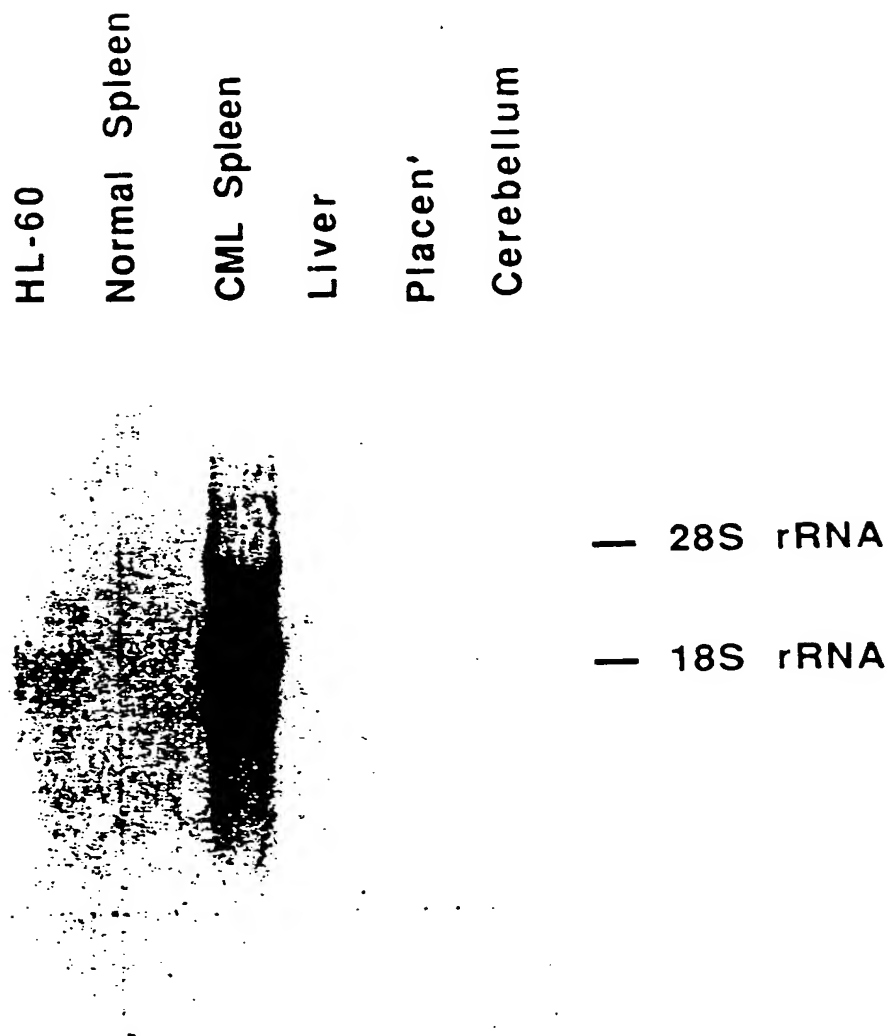


FIG. 7

